Amendments to the Specification:

Please replace the paragraph beginning at page 4, line 13 with the following amended paragraph:

The "percent identity" of two amino acid sequences is determined using the algorithm of Karlin and Altschul ((1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268), modified as in Karlin and Altschul ((1993) Proc. Natl. Acad. Sci. USA 90, 5873-5877). Such an algorithm is incorporated into the XBLAST programs of Altschul, et al. ((1990) J. Mol. Biol. 215, 403-410), available on the world wide web. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul, et al. ((1997) Nucleic Acids Res. 25, 3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST) are used. See www.ncbi.nlm.nih.gov.